

BLAST Basic Local Alignment Search Tool

•

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Blast 2 sequences

X98077:Saito_X2

Results for: ▼

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|1914699|emb|X98077.1|HBVCGWITY

Description

Hepatitis B virus complete genome, wild type

Molecule type

nucleic acid

Query Length

3215

Subject ID

14321

Description

None

Molecule type

nucleic acid

Subject Length

22

Program

BLASTN 2.2.20+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

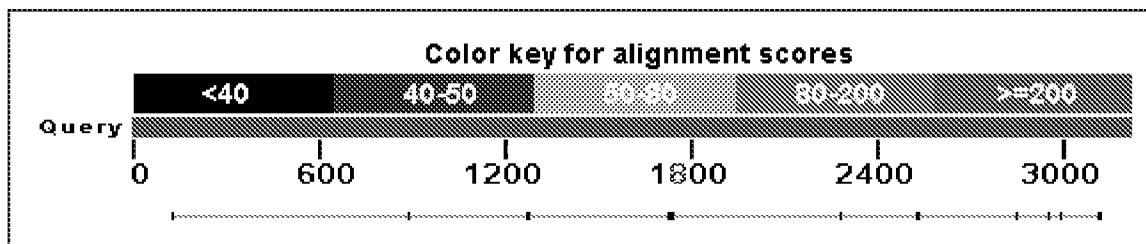
Effective search space 38460


[Graphic Summary](#)

Distribution of 12 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



[Dot Matrix View](#) 

Plot of gi|1914699|emb|X98077.1|HBVCGWITY vs 14321

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



[Descriptions](#)

Legend for links to other resources:  UniGene  GEO  Gene  Structure  Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

14321	26.5	186	2%	4e-04	100%

Alignments Select All Get selected sequences Distance tree of results

>lcl|14321
Length=22

Sort alignments for this subject seq
E value **Score** **Percent identity**
Query start position **Subject star**

Score = 26.5 bits (28), Expect = 4e-04
Identities = 16/17 (94%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query  1728  GAGTGGGAGGAGTTGGG  1744
          || |||||
Sbjct   6    GACTGGGAGGAGTTGGG  22
```

Score = 17.5 bits (18), Expect = 0.21
Identities = 9/9 (100%), Gaps = 0/9 (0%)
Strand=Plus/Plus

```
Query  893  GGAGTTGGG  901
          |||||
Sbjct  14   GGAGTTGGG  22
```

Score = 15.7 bits (16), Expect = 0.72
Identities = 8/8 (100%), Gaps = 0/8 (0%)
Strand=Plus/Plus

```
Query  1744  GGGAGGAG  1751
          |||||
Sbjct  10    GGGAGGAG  17
```

Score = 15.7 bits (16), Expect = 0.72
Identities = 8/8 (100%), Gaps = 0/8 (0%)
Strand=Plus/Minus

```
Query  2282  ACTCCTCC  2289
          |||||
Sbjct  18    ACTCCTCC  11
```

Score = 13.9 bits (14), Expect = 2.5
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Plus

```
Query  2992  AAGGACT  2998
          |||||
Sbjct   3    AAGGACT   9
```

Score = 13.9 bits (14), Expect = 2.5
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Plus

```
Query  133  GACTGGG  139
          |||||
Sbjct   6   GACTGGG  12
```

Score = 13.9 bits (14), Expect = 2.5
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Plus

Query 2849 TGGGAGG 2855
 |||||||
Sbjct 9 TGGGAGG 15

Score = 13.9 bits (14), Expect = 2.5
Identities = 9/10 (90%), Gaps = 0/10 (0%)
Strand=Plus/Minus

Query 3116 CAGCTCCTCC 3125
 || |||||
Sbjct 20 CAACTCCTCC 11

Score = 13.9 bits (14), Expect = 2.5
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Minus

Query 3122 CTCCTCC 3128
 |||||||
Sbjct 17 CTCCTCC 11

Score = 13.9 bits (14), Expect = 2.5
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Minus

Query 2531 AACTCCT 2537
 |||||||
Sbjct 19 AACTCCT 13

Score = 13.9 bits (14), Expect = 2.5
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Minus

Query 1277 AACTCCT 1283
 |||||||
Sbjct 19 AACTCCT 13

Score = 13.9 bits (14), Expect = 2.5
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Minus

Query 2954 CCAACTC 2960
 |||||||
Sbjct 21 CCAACTC 15

Select All [Get selected sequences](#) [Distance tree of results](#)